

General	Description	References	Comments	Links	Keywords	Sequence
-------------------------	-----------------------------	----------------------------	--------------------------	-----------------------	--------------------------	--------------------------

General information

Entry name	ATPG_HAEIN
Accession number	<u>P43716</u>
Created	Rel. 32, 1-NOV-1995
Sequence update	Rel. 32, 1-NOV-1995
Annotation update	Rel. 40, 16-OCT-2001

Description and origin of the Protein

Description	ATP SYNTHASE GAMMA CHAIN (EC <u>3.6.3.14</u>).
Gene name(s)	ATPG OR HI0480.
Organism source	Haemophilus influenzae.
Taxonomy	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus.
NCBI TaxID	<u>727</u>

References

- [1] Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A., Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J.-F., Dougherty,B.A., Merrick,J.M., McKenney,K., Sutton,G., Fitzhugh,W., Fields,C.A., Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.-I., Glodek,A., Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E., Cotton,M.D., Utterback,T.R., Hanna,M.C., Nguyen,D.T., Saudek,D.M., Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L., Geoghagen,N.S.M., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M., Smith,H.O., Venter,J.C.,
Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
(1995) *Science* 269:496

Position	SEQUENCE FROM N.A.
----------	--------------------

	Comments	STRAIN=RD / KW20 / ATCC 51907;
	Medline	<u>95350630</u>
	PubMed	<u>7542800</u>

Comments

FUNCTION	PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.
SUBUNIT	F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
SIMILARITY	BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.

Copyright

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Database cross-references

EMBL	U32730 ; AAC22138.1 ; -.
HSSP	P05631 ; 1BMF .
TIGR	HI0480 ; -.
InterPro	IPR000131 ; ATPase_gamma.
Pfam	PF00231 ; ATP-synt; 1.
PRINTS	PR00126 ; ATPASEGAMMA.
PROSITE	PS00153 ; ATPASE_GAMMA; 1.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome;

Sequence information

Length: **289 aa**, molecular weight: **32069 Da**, CRC64 checksum: **622CBA682F37FD00**

```

MAGAKEIKTK IASVQSTQKI TKAMEMVATS KMRKTQDRMA ASRPYSETIR NVISHVSKAS      60
IGYKHPFLVE REVKKIGILV ISTRGMCGG LNVNLFKTTL NQIKNWKEQN ISTDGLIGS      120
KGISFFRSFG FNIKGQLSGL GDTPALEELI GVANTMFDAY RGEIDAVYI AYNKFVNTMS      180
QKPVVQQLVP LPESKDDHLN ERQQTWDYLY EPEPKVLLDS LLVRYLESQI YQAVVDNVAS      240
EQAARMVAMK AATDNAGNLI NDLRLVYNKA RQASITNELN EIVAGAAAI      289

```

//

General	Description	References	Comments	Links	Keywords	Sequence
-------------------------	-----------------------------	----------------------------	--------------------------	-----------------------	--------------------------	--------------------------

ATP synthase gamma subunit

Accession	IPR000131; (ATPase_gamma) matches 100 proteins
FullName	ATP synthase gamma subunit
Type	Domain
Signatures	PRINTS: PR00126 <i>ATPASEGAMMA</i> PROSITE: PS00153 <i>ATPASE_GAMMA</i> PFAM: PF00231 <i>ATP-synt</i>
Molecular Function	hydrogen-transporting two-sector ATPase (GO:0003936)
Biological Process	hydrogen transport (GO:0006818)
Cellular Component	membrane (GO:0016020)
Abstract	<p>ATP synthase (proton-translocating ATPase) [EC:3.6.1.34] [1, 2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis.</p>
Examples	<p>P36542 P00837 P29790</p> <p>View Signature matches on the examples</p>
	<ol style="list-style-type: none"> 1. Futai,M., Noumi,T., Maeda,M., ATP synthase (H⁺-ATPase) - Results by combined

References	<p>biochemical and molecular biological approaches. (1989) <i>Annu. Rev. Biochem.</i> 58: 111-136 [MEDLINE:89372792] [PUB00000063]</p> <p>2. Senior,A.E., ATP synthesis by oxidative phosphorylation. (1988) <i>Physiol. Rev.</i> 68: 177-231 [MEDLINE:88097736] [PUB00004515]</p> <p>3. Futai,M., Maeda,M., Miki,J., Mukohata,Y., The gamma-subunit of ATP synthase from spinach chloroplasts - primary structure deduced from the cloned CDNA sequence. (1988) <i>FEBS Lett.</i> 232: 221-226 [MEDLINE:88211863] [PUB00001558]</p>
Database links	BLOCKS: IPB000131 ; PDOC: PDOC00138 ;
Matches	Table all Graphical all

1. *Science*. 1995, 269 (5223):496-512

Related Articles by NCBI

Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

Fleischmann,R D. , Adams,M D. , White,O. , Clayton,R A. , Kirkness,E F. ,
Kerlavage,A R. , Bult,C J. , Tomb,J F. , Dougherty,B A. , Merrick,J M.

Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.

An approach for genome analysis based on sequencing and assembly of unselected pieces of DNA from the whole chromosome has been applied to obtain the complete nucleotide sequence (1,830,137 base pairs) of the genome from the bacterium *Haemophilus influenzae* Rd. This approach eliminates the need for initial mapping efforts and is therefore applicable to the vast array of microbial species for which genome maps are unavailable. The *H. influenzae* Rd genome sequence (Genome Sequence DataBase accession number L42023) represents the only complete genome sequence from a free-living organism.

MedlineID: 95350630

PMID: 7542800

ISSN: 0036-8075

Publication Type:

Journal Article

Substances:

Bacterial Proteins

DNA, Bacterial

RNA, Bacterial

RNA, Ribosomal

1. *Science*. 1995, 269 (5223):496-512

Related Articles by NCBI

Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

Fleischmann,R D. , Adams,M D. , White,O. , Clayton,R A. , Kirkness,E F. , Kerlavage,A R. , Bult,C J. , Tomb,J F. , Dougherty,B A. , Merrick,J M.

Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.

An approach for genome analysis based on sequencing and assembly of unselected pieces of DNA from the whole chromosome has been applied to obtain the complete nucleotide sequence (1,830,137 base pairs) of the genome from the bacterium *Haemophilus influenzae* Rd. This approach eliminates the need for initial mapping efforts and is therefore applicable to the vast array of microbial species for which genome maps are unavailable. The *H. influenzae* Rd genome sequence (Genome Sequence DataBase accession number L42023) represents the only complete genome sequence from a free-living organism.

MedlineID: 95350630

PMID: 7542800

ISSN: 0036-8075

Publication Type:

Journal Article

Substances:

Bacterial Proteins

DNA, Bacterial

RNA, Bacterial

RNA, Ribosomal

ID AR089428 standard; DNA; UNC; 1374 BP.
 XX
 AC AR089428;
 XX
 SV AR089428.1
 XX
 DT 12-SEP-2000 (Rel. 65, Created)
 DT 12-SEP-2000 (Rel. 65, Last updated, Version 1)
 XX
 DE Sequence 187 from patent US 5994066.
 XX
 KW .
 XX
 OS unidentified
 OC unclassified.
 XX
 RN [1]
 RP 1-1374
 RA Bergeron M.G., Picard F.J., Ouellette M., Roy P.H.;
 RT "Species-specific and universal DNA probes and amplification primers to
 RT rapidly detect and identify common bacterial pathogens and associated
 RT antibiotic resistance genes from clinical specimens for routine diagnosis
 RT in microbiology laboratories";
 RL Patent number US5994066-A/187, 30-NOV-1999.
 XX

FH Key Location/Qualifiers
 FH
 FT source 1..1374
 FT /db_xref="taxon:32644"
 FT /organism="unidentified"
 XX

SQ Sequence 1374 BP; 425 A; 238 C; 312 G; 399 T; 0 other;
 atgtcagcag gaaaaattgt acaaatcatc ggtgcggtga ttgacgttga atttccacaa 60
 gatgcagtgc caaaagttaa cgatgcatta aaagttgaat caggtttaac acttgaggtg 120
 caacaacaat taggtggcgg agtagttcgt tgtattgcat tgggtacatc tgatggttta 180
 aaacgtggct taaaagtaga aaacacaaat aaccaattc aagtaccagt aggcacaaaa 240
 acacttggtc gtattatgaa tgtgttgggc gaaccaattg acgaacaagg agcaattggt 300
 gaagaagagc gttgggctat ccaccgttcg gcaccgagct atgaagaaca atcaaacagt 360
 acggaattat tagaaactgg tatcaaagtg atcgacttaa tttgtccatt cgcaaaaggt 420
 ggtaaaagttg gtttattcgg cgggtgcaggt gtaggtaaaa ccgtaaatat gatggagttg 480
 attcgttaata ttgcgattga gcattcaggt tactctgtat ttgcgggtgt aggcgaacgt 540
 actcgtgaag gtaatgactt ctatcatgaa atgaaagatt ctaacgtatt agataaagta 600
 tcttttggtt atggtcaaat gaacgagcca ccaggtaacc gtttacgtgt tgcattgact 660
 ggtttaacta tggctgaaaa attccgtgat gaaggtcgag atgtattatt ctttgtggat 720
 aatatctatc gttataccct tgctggtacg gaagtatctg cgttattagg tcgtatgcca 780
 tccgcggtag gttaccaacc gacattggca gaagaaatgg gtgtgttaca agaacgtatc 840
 acttcaacca aaacaggttc tatcacttct gtgcaagcgg tgtacgtacc agcggatgac 900
 ttaactgacc catctccagc aacaactttc gcacatttag actcaactgt tgtattaagt 960
 cgtcaaatcg catctttagg tttttaccct gcagttgatc cattagattc aacttcacgt 1020
 cagctagacc cgcttggtgt tggtaagaa cattatgatg ttgctcgtgg tgtacaaggt 1080
 attttacaac gttataaaga attgaaagat attatcgcaa ttcttggtat ggatgaatta 1140
 tctgaagaag ataaactagt ggtagcacgt gcacgtaaaa ttgaacgttt cttatcacia 1200
 ccattctttg ttgcagaagt cttcacaggt tcaccaggta aatacgtgac attaaaagac 1260
 accatccgtg gcttcaaagg tatcttagat ggccaatatg accatattcc tgaacaagcg 1320
 ttctatatgg ttggttcaat cgatgaagtg ttagaaaaag ccaaaaatat gtaa 1374

//

ID HI32730 standard; DNA; PRO; 13828 BP.
 XX
 AC U32730; L42023;
 XX
 SV U32730.1
 XX
 DT 09-AUG-1995 (Rel. 44, Created)
 DT 15-JUN-1998 (Rel. 56, Last updated, Version 9)
 XX
 DE Haemophilus influenzae Rd section 45 of 163 of the complete genome.
 XX
 KW .
 XX
 OS Haemophilus influenzae Rd
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus;
 OC Haemophilus influenzae.
 XX
 RN [1]
 RP 1-13828
 RX MEDLINE; 95350630.
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F.,
 RA Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.,
 RA Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D.,
 RA Fritchman J.L., Fuhrmann J.L., Geoghagen N.S., Gnehm C.L., McDonald L.A.,
 RA Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd";
 RL Science 269(5223):496-512(1995).
 XX
 RN [2]
 RP 1-13828
 RX MEDLINE; 96398784.
 RA Tatusov R.L., Mushegian A.R., Bork P., Brown N.P., Hayes W.S.,
 RA Borodovsky M., Rudd K.E., Koonin E.V.;
 RT "Metabolism and evolution of Haemophilus influenzae deduced from a
 RT whole-genome comparison with Escherichia coli";
 RL Curr. Biol. 6(3):279-291(1996).
 XX
 RN [3]
 RP 1-13828
 RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
 RT ;
 RL Submitted (25-JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
 RL 20850, USA
 XX
 RN [4]
 RP 1-13828
 RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
 RT ;
 RL Submitted (27-SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
 RL 20850, USA
 XX
 RN [5]
 RP 1-13828
 RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J.,
 RA Hickey E., Dodson R., Gwinn M.;
 RT ;
 RL Submitted (28-MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
 RL 20850, USA
 XX

DR SWISS-PROT; O86225; Y48A_HAEIN.
 DR SWISS-PROT; P43714; ATPA_HAEIN.
 DR SWISS-PROT; P43715; ATPB_HAEIN.
 DR SWISS-PROT; P43716; ATPG_HAEIN.
 DR SWISS-PROT; P43717; ATPD_HAEIN.
 DR SWISS-PROT; P43718; ATP_E_HAEIN.
 DR SWISS-PROT; P43719; ATP6_HAEIN.
 DR SWISS-PROT; P43720; ATPF_HAEIN.
 DR SWISS-PROT; P43721; ATPL_HAEIN.
 DR SWISS-PROT; P44002; Y476_HAEIN.
 DR SWISS-PROT; P44327; HIS7_HAEIN.
 DR SWISS-PROT; P44340; HIS5_HAEIN.
 DR SWISS-PROT; P44423; HIS8_HAEIN.
 DR SWISS-PROT; P44434; HIS2_HAEIN.
 DR SWISS-PROT; P44435; HIS4_HAEIN.
 DR SWISS-PROT; P44436; HIS6_HAEIN.
 DR SWISS-PROT; P44727; TYRP_HAEIN.

XX

FH Key Location/Qualifiers

FH

FT source

1..13828

FT /db_xref="taxon:71421"

FT /organism="Haemophilus influenzae Rd"

FT CDS

65..1168

FT /codon_start=1

FT /db_xref="SWISS-PROT:P44423"

FT /note="similar to SP:P06986 GB:U02071 GB:X03416 PID:41695

FT PID:41710 percent identity: 60.40; identified by sequence

FT similarity; putative"

FT /transl_table=11

FT /gene="HI0470"

FT /product="histidinol-phosphate aminotransferase (hisC)"

FT /protein_id="AAC22129.1"

FT /translation="MNDYNHILQWKKTIMTITTLRQNIQALTPYQSARKLGGNGTIW

FT LNANEYPTSPFEQLSGKDLNRYPEPQPQRVVQAYANYAGVSTENVLVTRGGDEGIELII

FT HTFCEPKQDAILFCPPTYGMYAVSAETAGVLSKTVPLTDDFQNLNPEIKNHLNDVKVVF

FT VCSPNNPTGNLLKQSDILDLLQITAGKAIVVVDEAYIEFCPEASVINLLKNYPHLAIIR

FT TLSKAFALAGLRGCVLANPELIDILSKVIAPYPIPVPSADLAEQALRPSNIATVQALT

FT QELLSNRQWLAKALLVLHQVEKVESEANYLLIKCQNGQAVFKALWEQGIILRDQNKTL

FT HLQNCIRITVGTRECEKVVEAIKEVK"

FT CDS 1280..2368

FT /codon_start=1

FT /db_xref="SWISS-PROT:P44327"

FT /note="similar to SP:P06987 GB:X03416 PID:41696 PID:41711

FT GB:U00096 percent identity: 64.97; identified by sequence

FT similarity; putative"

FT /transl_table=11

FT /gene="HI0471"

FT /product="imidazoleglycerol-phosphate dehydratase /

FT histidinol-phosphatase (hisB)"

FT /protein_id="AAC22130.1"

FT /translation="MQPTLFIDRDGTLIDEPKTDFQIDSLEKLKLEPKVIPALLRLKAK

FT YRFVIVSNQDGLGTDAFPQTDFDKPHNVMMALFESQGITFDEVLCIPHKPEENCLCRKP

FT KIKLLDHYIRKNLFDIDRSFVIGDRETDVQLAENLGIRAIQYDPQKMNWDLIAEKLLGE

FT TVTNCGRKPPRFAEVIRQTKETDIKVQVWLDEAGVNEIKTGVGFFDHMLDQIATHGGFR

FT MNVQCKGDLWIDEHHTVEDTALALGQALKQAVGDKRGIARFGFVLPMECKAEACALDLS

FT GRPWIKFNACFKRDKVGDFSTELTEHFFQSLAFSMLATLHLNVTGNNDHHKIESLFKAF

FT GRTLRLQAIRIEGNEMPSSKGVL"

FT CDS 2434..3033

FT /codon_start=1

FT /db_xref="SWISS-PROT:P44340"

FT /note="similar to SP:P10375 PID:41712 GB:U00096 PID:1736701

FT PID:1736710 percent identity: 55.90; identified by sequence

FT similarity; putative"

FT /transl_table=11

```

FT      /gene="HI0472"
FT      /product="amidotransferase (hisH)"
FT      /protein_id="AAC22131.1"
FT      /translation="MINITIIDTGCANLSSVKFAFDRLGYNTEITFDLNKIKSADKLIL
FT      PGVGTANAAMYNLQERQLIETIQNLTPVLGICLGMQLMTEFSEEGNVPTNLNISGKTN
FT      RIPDTGLPLPQMGWNRVQFVKNCPLFDGIVQNSHFYFVHSYAVSPNEHSVAISNYGVNF
FT      SAAIAKENFYGVQFHPERSGKNGALLLNKFVEKVPF"
FT      CDS      3069..3818
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P44435"
FT      /note="similar to SP:P10371 PID:41713 GB:U00096 PID:1736702
FT      PID:1736711 percent identity: 62.86; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0473"
FT      /product="phosphoribosylformimino-5-aminoimidazole
FT      carboxamide ribotide isomerase (hisA)"
FT      /protein_id="AAC22132.1"
FT      /translation="MKQSITIPALDLINGQVVRHLHQGDYAKQTTYSNPIKQFDNYVRQ
FT      GAKQLHLVDLTGAKNPQSRQTALIGKIVEATQCKVQVGGGIRTEQDVADLLAVGANRVV
FT      IGSTAVTHRSMVKNWFIKYGAKEFVLALDVNINASGQKIVAISGWQEEESGVLLTIED
FT      FQTVGLQQVLCTDISRDGTLTGSNIGLYQEICEKYPPIQFQSSGGIGSLADIEALKGTG
FT      VSGVIVGRALLEGKFTLSEAIKCWQNG"
FT      CDS      3800..4576
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P44436"
FT      /note="similar to SP:P10373 PID:41714 PID:598474 GB:U00096
FT      PID:1736704 percent identity: 82.03; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0474"
FT      /product="hisF cyclase (hisF)"
FT      /protein_id="AAC22133.1"
FT      /translation="MLAKRIIPCLDVRDQGVVKGQVFRNHEIIGDIVPLAQRYAQEGAD
FT      ELVFYDITASDGRITVDKSWVERIAQVIDIPFCVAGGIKTIEDAEKLFAFGADKISINS
FT      PALADPTLISRLADRFGVQAIIVGIDSWFEQETGKYWVNQYTGDETRTRQTHWQLLDWV
FT      KEVQQCGAGEIVLNMNQDGLRNGYDLAQLKLVRGVCRVPLIASGGAGKMVHFRDAFIE
FT      AKVDGALAASVFHKQIIEIGELKSYLVQSAIEIRSE"
FT      CDS      4576..5241
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P44434"
FT      /note="similar to SP:P06989 GB:D43637 GB:U02072 GB:X03974
FT      PID:41700 percent identity: 61.22; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0475"
FT      /product="phosphoribosyl-AMP cyclohydrolase /
FT      phosphoribosyl-ATP pyrophosphohydrolase (hisIE)"
FT      /protein_id="AAC22134.1"
FT      /translation="MNITKIDWQKVNGLLPVIIQNISTREVLMLGYMNEEALTKTIKER
FT      KVTFFSRTKQRLWTKEISGNFLNVEEMSLDCDNDTLLILVDPIGATCHTGEYSCFHQF
FT      TSPQSENKKQQFANWAWFIKLEQHLKEKKNADPSNSYTATLHAKGTTKIAQKVGEEGVE
FT      TALAAVAQDKAEVISEATDLVYHLTVLLHNQDLQWYEIIAKLQERHQGIGLHPEGGNK"
FT      CDS      5323..5475
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P44002"
FT      /note="hypothetical protein; identified by GeneMark;
FT      putative"
FT      /transl_table=11
FT      /gene="HI0476"
FT      /product="H. influenzae predicted coding region HI0476"
FT      /protein_id="AAC22144.1"
FT      /translation="MVIKCIDKQQNLGNIILFLLKQQYSKEDSKKFTIYKFYLQTVNY
FT      TIQLS"
FT      CDS      5505..6707

```

```

FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P44727"
FT      /note="similar to GB:M23240 SP:P18199 PID:148089 GB:U00096
FT      PID:1736569 percent identity: 47.24; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0477"
FT      /product="tyrosine-specific transport protein (tyrP)"
FT      /protein_id="AAC22135.1"
FT      /translation="MNKTVGSTLLVAGTMIGAGMLAMPLTSAGIGFGFTLVLLLGLWAL
FT      LTFSAALLFVELYQTAESDAGIGTLAEQYFGKTGRIIATAVLIIFLYALIAAYISGGGSL
FT      LKDLLPESFGDKVSULLFTVIFGSFIVIGTHSVDKINRVLFFVMLAAFAVVLSTMLPEI
FT      KFDNLMATPIDKALIIASPVFFTAFGFHGSIPSLNKYLDGNVKALRFSILVGSAILTC
FT      AYILWQLSTHGLLTQNEFLQILKEDATLNLGVKATFAITGSNVIASAVKLFSTLALITS
FT      FLGVGLGLLECIEDLLKRSFNVTAGRISLGLLTFIPPLVFALFYPEGFILALGYAGQMF
FT      AFYAVVLPVSLVWKARRAHANLPYKVGWGNLTLIIIVLVGLVITSIPFAIRAGYLPFVVG"
FT      complement(6893..7321)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43718"
FT      /note="similar to GB:L10328 SP:P00832 GB:M25464 GB:V00267
FT      GB:V00311 percent identity: 59.56; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0478"
FT      /product="ATP synthase F1, subunit epsilon (atpC)"
FT      /protein_id="AAC22136.1"
FT      /translation="MATFNLTIVSAEQKIFEGEVKQIQVTGVEGELGILPGHTPLLTAI
FT      KPGIVKFTLKDGNEEVIYVSGGFLEVQPNIVTVLADIAIRGSELDADRIHEAKRKAEN
FT      IVSRGSDADHDLLVAKLSKELAKLRAYELTEKLLKTRR"
FT      complement(7351..8724)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43715"
FT      /note="similar to GB:L10328 SP:P00824 GB:M25464 GB:V00267
FT      GB:V00311 percent identity: 89.30; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0479"
FT      /product="ATP synthase F1, subunit beta (atpD)"
FT      /protein_id="AAC22137.1"
FT      /translation="MSAGKIVQIIIGAVIDVEFPQDAVPKVDALKVESGLTLEVQQQLG
FT      GGVVRCIALGTSGLKRGKVENTNPNPIQVPVGTKTGLRIMNVLGEPIDEQGAIGEEER
FT      WAIHRSAPSYEEQSNSTELLETGIKVIDLICPFAKGGKVGLFGGAGVGKTVNMELIRN
FT      IAIHSGYSVFAGVGERTREGNDFYHEMKDSNVLDKVS LVYGQMNEPPGNRLRVALTGL
FT      TMAEKFRDEGRDVLFFVDNIYRYTLAGTEVSALLGRMPSAVGYPPTLAEEMGVLQERIT
FT      STKTGSITSVQAVYVPADDLTDPSPATTFHAHLDSTVVLSRQIASLGIYPAVDPLDSTSR
FT      QLDPLVVGQEHYDVARGVQGIQRYKELKDIIAILGMDELSEEDKLVARARKIERFLS
FT      QPFFVAEVFTGSPGKYVTLDKTIIRGFKGILDGEYDHIPEQAFYMGVSIDEVLEKAKNM"
FT      complement(8741..9610)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43716"
FT      /note="similar to GB:L10328 SP:P00837 GB:M25464 GB:V00267
FT      PID:146324 percent identity: 65.28; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0480"
FT      /product="ATP synthase F1, subunit gamma (atpG)"
FT      /protein_id="AAC22138.1"
FT      /translation="MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPY
FT      SETIRNVISHVSKASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIK
FT      NWKEQNISTDGLIGSKGISFFRSFGFNKQQLSGLGDTPALEELIGVANTMFDAYRNG
FT      EIDAVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLL
FT      VRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNE
FT      IVAGAAAI"
FT      complement(9626..11167)

```

```

FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43714"
FT      /note="similar to GB:L10328 SP:P00822 GB:M25464 GB:V00265
FT      GB:V00266 percent identity: 86.55; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0481"
FT      /product="ATP synthase F1, subunit alpha (atpA)"
FT      /protein_id="AAC22139.1"
FT      /translation="MQLNSTEISELIKRIQFDVVSEARNTGTIVSVSDGIIRIHGLS
FT      DVMQGEMIALPGNRYAMALNLERDSVGAVVMGPYADLAEGMEVQCTGRILEVPVGRGLL
FT      GRVVNTLGQPIDGKEIENDGFSPEVIAPGVIDRRSVDQPVQGTGYKAVDSMVPIGRGQ
FT      RELIIGDRQTGKTALDAIINQRNSGIKCIYVAIGQKASTIANVVRKLEEHGALANTI
FT      VVAASASESAALQYLAPYAGCAMGEYFRDRGEDALIVYDDLKQAVAYRQISLLLRPP
FT      GREAYPGDVFYLSRLLERASRVNEDYVEKFTKGEVKGKTGSLTALPIIETQAGDVSAF
FT      VPTNVISITDQIFLESNLFNSGIRPAVNPGISVSRVGGSAQTKVIKKLAGGIRITALAQ
FT      YRELAFAQFASDLDDATRKQLSHGEKVTELLKQKQFTPLSVAEQAVILFAVEFGYLLD
FT      VELSKIASFETALLDYSNRNHAEFMQELNKTGNYNDEIKDTLKSILDGFKANSAW"
FT      CDS      complement(11180..11713)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43717"
FT      /note="similar to GB:L10328 SP:P00831 GB:M25464 GB:V00264
FT      GB:V00266 percent identity: 57.95; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0482"
FT      /product="ATP synthase F1, subunit delta (atpH)"
FT      /protein_id="AAC22140.1"
FT      /translation="MSELTTIARPYAKAAFDFAIEQSAVEKWTEMLGFAAAVAEDEVK
FT      AYLSSSSLSAQKLADTVISICGEQLDQYGQNLIRLMAENKRLSAIPAVFEEFKHHVEEHQ
FT      AIAEVEVTSAPLNATQIEKIAAAMEKRLARKVKLNCNVDNALIAGVIVRTEDFVIDGS
FT      SRGQLTRLANELQL"
FT      CDS      complement(11726..12196)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43720"
FT      /note="similar to GB:L10328 SP:P00859 GB:M10422 GB:M25464
FT      GB:V00264 percent identity: 63.46; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0483"
FT      /product="ATP synthase F0, subunit b (atpF)"
FT      /protein_id="AAC22141.1"
FT      /translation="MNLNATLIGQLIAFALFVWFCMKFVWPPIINAIETRQSQIANALA
FT      SAEAAKKEQADTKNLVEQELSAKQLAQDILDAANKRRNEVLDEVKAEAEELKAKIIAQ
FT      GYAEVEAERKRVQEELRLKVASLAVAGAEKIVGRSIDEAANNDIIDKLVAEL"
FT      CDS      complement(12246..12500)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43721"
FT      /note="similar to SP:P12991 PID:48334 percent identity:
FT      62.65; identified by sequence similarity; putative"
FT      /transl_table=11
FT      /gene="HI0484"
FT      /product="ATP synthase F0, subunit c (atpE)"
FT      /protein_id="AAC22142.1"
FT      /translation="METVITATIIGASILLAFALGTAIGFAILGGKFLESSARQPELA
FT      SSLQTKMFIVAGLLDAIAMIAVGISLLFIFANPFIIGLLN"
FT      CDS      complement(12556..13344)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:P43719"
FT      /note="similar to GB:L10328 SP:P00855 GB:M14019 GB:M25464
FT      GB:M29174 percent identity: 58.17; identified by sequence
FT      similarity; putative"
FT      /transl_table=11
FT      /gene="HI0485"
FT      /product="ATP synthase F0, subunit a (atpB)"

```

```

FT      /protein_id="AAC22143.1"
FT      /translation="MSGQTTSEYISHHLSFLKTGDGFNVHIDTLFFSILAAVIFLQVF
FT      SRVGKKATTGVPQKMQCLVEIVVEVWNGIVKENFHGPRNVVAPLALTI FCWVFIMNAID
FT      LIPVDFLPQFAGLFGIHYLRVPTADISATLGMSICVFFLILFYTIKSKGFKGLVKEYT
FT      LHPFNHWAFIPVNFIEITVTLAKPISLAFRLFGNMYAGELIFILIAVMSANMAIAL
FT      GIPLHLAWAIFHILVITLQAFIFMMLTVVYLSIAYNKADH"
FT      CDS complement(13381..13755)
FT      /codon_start=1
FT      /db_xref="SWISS-PROT:O86225"
FT      /note="Brute Force ORF; identified by GeneMark; putative"
FT      /transl_table=11
FT      /gene="HI0485.1"
FT      /product="H. influenzae predicted coding region HI0485.1"
FT      /protein_id="AAC22145.1"
FT      /translation="MSRILSHAKKNYRKAIVIESLLLVVFYLLIYGWQRQSAVDFSYG
FT      LSAFLPFCTFIIFIRKQNFSTKLTAIYRAEAIKFILTMVFIIIAIKWLFVINFIADF
FT      VGFLALVLNNIPLILNKI"
XX
SQ

```

Sequence 13828 BP; 4368 A; 2718 C; 2562 G; 4180 T; 0 other;

ttaattatag	atctaagcac	gacacgtaag	cagtcaaatt	ttcatacaac	aatacgaat	60
atgtatgaat	gattacaatt	cgcacat	ttt	acaatggaag	aaaacaataa	120
aactttatcc	cgacaaaata	tacaagcctt	aacgccatat	caatccgctc	gaaaactcgg	180
cggcaatggt	acgatttggc	tgaatgcaa	tgaatatcca	acttcgcctg	aatttcagct	240
ttcgggtaag	gatttaaacc	gctaccccg	acctcagcct	caaagagtgg	tacaggctta	300
tgcgaattat	gcgggcgttt	caactgaaaa	tgtactcggt	actcgtggcg	gtgatgaagg	360
cattgaattg	ataatccaca	ctttttgcga	acccaaacaa	gatgccattt	tattctgtcc	420
tccgacttac	ggaatgtatg	cagtgagtgc	tgaacggca	ggtgtgctaa	gtaagaccgt	480
gcctttaact	gacgattttc	agcttaattt	gccagaaatc	aaaaatcatc	ttaatgatgt	540
aaaagtagtc	tttgtatgca	gcccaaataa	tccgacaggt	aatttgctca	agcaatcaga	600
tatactcgat	cttttgcaaa	tcacggcagg	caaagcgatt	gtggtggtgg	acgaagccta	660
tattgagttc	tgtcctgaag	caagcgttat	taatttgctt	aaaaattatc	cgcacttagc	720
aattatccgc	acgctctcta	aagcctttgc	tttagctgga	ttgcgtttgtg	gttttgtgtt	780
agcaaacctc	gagctaattg	acatcttaag	taaggtaatc	gctccatatac	ctatccctgt	840
gccgagtgtc	gatcttgcgg	aacaagcgtt	aagaccttcg	aacatcgcca	ctgttcaagc	900
tctcacacaa	gaacttcttt	ccaatcgta	atggcttgc	aaagctcttt	tagttttaca	960
tcaagtggaa	aaagtgtatg	aaagtgaagc	taattatctg	ttgatcaaat	gtcaaaacgg	1020
gcaagctgtg	tttaaggcat	tgtgggaaca	aggaattatt	ttaagagacc	agaataagac	1080
attgcattta	caaaattgta	ttcgcatatc	tgtgggaaca	aggaatgagt	gtgagaaagt	1140
tgttgaagca	attaaggagg	taaaatgaac	cacctcctat	ttaagtcaca	gagcgattcg	1200
agattattta	gttttatact	gtttgtataa	agcaaatgat	aaacctcata	ccattcataat	1260
aacattacacg	gagaaaaata	tgcaacctat	cttttttatc	gaccgagacg	gcacattaat	1320
tgatgaacca	aaaactgatt	tccaaattga	cagtttagag	aaactaaaaat	tagaaccgaa	1380
agtgattccc	gcactcctca	gactgaaagc	gaaataccgt	tttgtgatag	tttctaatac	1440
agatgggctt	ggtacggatg	cttttccgca	aacagatttt	gataagcccc	acaatgtaat	1500
gatggcatta	tttgaatctc	agggcattac	ctttgatgaa	gtactcattt	gcccgcataa	1560
gcccgaagaa	aattgtctat	gtcgcaaac	aaaaattaa	ttgcttgatc	actatatctg	1620
taaaaattta	ttcgatattg	accgctcttt	tgtcattggt	gaccgagaga	ccgatgtgca	1680
attagcagaa	aatctaggta	ttcgagctat	tcaatacgat	ccacagaaaa	tgaattggga	1740
tctgattgca	gaaaaattgt	tgggggaaac	ggtcacaaac	tgtggcaaac	gtccgccacg	1800
ttttgcagaa	gtaattcgct	aaactaaaga	gaccgatatt	aaagtgcagg	tttggctaga	1860
tgaagctggt	gtaaatgaaa	tcaaaaccgg	cgttggtttt	tttgaccata	tgctcgatca	1920
aatcgccaca	cacggtgggt	ttagaatgaa	cgtagcagtg	aaaggcgatt	tatggattga	1980
cgaacatcac	acggtggagg	acaccgctct	cgcccttgga	caagcactga	aacaagccgt	2040
tggtgacaaa	cggtgtattg	cccgtttcgg	ctttgtgctt	ccaatggacg	aatgtaaagc	2100
agaatgtgct	ttagatttat	cgggcagacc	ttggatcaaa	ttcaatgcct	gctttaaacg	2160
cgataaagt	ggcgatttta	gtacggaact	cactgaacat	ttctttcaat	ctttggcatt	2220
ttcaatgctt	gccacgcttc	atttaaatgt	cacaggtaat	aacgatcatc	ataaaataga	2280
gagcttattt	aaagcctttg	ggagaacatt	aagacaggcg	attcggattg	aaggaaatga	2340
aatgccaaagt	tcaaaaggag	ttttatagtt	gaaagagcgg	ttaatttttg	tcgtattttt	2400
gcaaaattcg	accgattgta	aaaggataaa	aaaatgataa	acatcacgat	tatagacaca	2460
ggttgtgcca	acctttcttc	tgtaaaattc	gcctttgacc	gattagggtta	caataccgag	2520
atcacttttg	atctcaataa	aatcaaatct	gccgataagc	tgattttacc	tggcgtaggc	2580
actgcaaatg	cagcaatgta	taattttaca	gaacgtcaat	tgatcgagac	cattcaaaat	2640
ctaacacaac	cagtgttagg	aatttgtttg	ggtatgcagt	taatgaccga	attttccgaa	2700
gagggtaagt	tgccgacctt	aaaccttaata	agcggaaaaa	ctaatacgaat	tcccgatagc	2760

ggtttacggt	tacctcaaat	gggatggaat	cgcggtgcaat	ttgtaaaaaa	ctgtccggtta	2820
tttgatggta	ttgtgcaaaa	tagtcacttc	tattttgtgc	atagttatgc	agtttagcccg	2880
aatgaacatt	cgggtggcaat	aagcaattat	gggtgtgaatt	tttctgctgc	gatagcgaaa	2940
gagaattttt	acggtgtaca	atttcaccc	gaacgttcg	gtaaaaatgg	tgcgttggtg	3000
ctaaaaaatt	ttgtggaaaa	agtaccgttt	taatcactag	atcatatagt	catacaggat	3060
caaacacaat	gaaacaatct	attattattc	ctgctcttga	tcttatcaat	ggtcaagttg	3120
tgcggttaca	ccaaggcgat	tatgccaa	aaactaccta	ttctgacaat	ccaattaa	3180
aatttgataa	ttatgtacgt	caaggagcaa	aaacaactca	tctagtcgat	ttaacgggag	3240
cgaaaaatcc	ccagtcaaga	caaaccgcac	ttattggaaa	aatcggtgaa	gcaacacaat	3300
gtaaagtaca	agtgaggga	ggcattcgta	cagagcaaga	tgtggcagat	ttattggctg	3360
tgggtgcgaa	tcgctgggtg	attggttcaa	ccgccgtaac	tcatcgttca	atggtgaaaa	3420
actggttcac	caaatatggt	gcggaaaaat	ttgttctagc	attagacgtg	aatattaatg	3480
caagcgggtca	gaaaatcggt	gcgattagcg	gttggcagga	agaaagtgg	gtactattag	3540
aaacgttgat	cgaagatttc	caaaccgttg	gcttacaaca	agttttatgt	accgatattt	3600
cacgcgatgg	caccttgaca	ggttcaaata	ttggacttta	tcaagaaatt	tgtgagaatt	3660
atccacctat	tcagtttcaa	tcttctggag	ggattggttc	actggctgat	attgaggctc	3720
taaaaggcac	aggtgtgtca	ggtgtaattg	taggtcgagc	tttattagaa	ggaaaattta	3780
cgctttcggg	ggcaatcaaa	tgttggcaaa	acggataatt	ccttgttttg	atgtacgtga	3840
tggacaggtg	gtaaaagggg	tacaattccg	taaccacgaa	attattggcg	atattgtgcc	3900
acttgctcaa	cgctatgcgc	aagaaggagc	tgatgaattg	gtattttatg	atattacggc	3960
ttcatcagac	ggtcgtaccg	tggataaaa	ttgggtagaa	cgaatcgctc	aggttaattga	4020
tattccggtt	tgcgtagcag	gtgggattaa	aaccattgaa	gatgcggaaa	aattgtttgc	4080
atttggggcg	gataaaattt	cgattaattc	ccctgctctc	gctgatccaa	cgctcatttc	4140
tcgcttagca	gatcgttttg	gcgtacaagc	gattgtagta	ggtattgata	gttggtttga	4200
acaggaacaa	ggtaagtatt	gggtaaacca	atatacaggc	gatgaaacac	gtacccgaca	4260
aactcattgg	cagttgttag	attgggtaaa	agaagtacaa	caatgcggtg	caggagaaat	4320
cgtgctaaat	atgatgaatc	aagatggttt	acgaaacggg	tacgatttag	cccagctcaa	4380
gctggtgcga	ggagtatgta	gagtacctct	aattgcatct	ggcgggtgcg	gtaaaatggt	4440
acattttcgt	gatgctttta	ttgaagcaaa	agtagatggg	gcattagctg	ccagcgtatt	4500
ccataaacag	attattgaaa	ttggcgagtt	aaaatcctac	cttgtgcaat	cagccatcga	4560
gattcggagt	gaataatgaa	tattactaaa	atagactggc	aaaaagttaa	tggctcttct	4620
cctgttatta	ttcaaatata	aagtactcgt	gaggtactaa	tgcttggtta	tatgaatgaa	4680
gaagccctta	caaaaaccat	caagaacagt	aaagtaactt	tcttctctcg	taccaacaaa	4740
cgattatgga	caaaaggaga	aatctcgggc	aattttttta	atgtggaaga	aatgagctta	4800
gattgcgata	acgacacttt	gctcatttta	gttgatccca	ttggggcaac	ttgccacaca	4860
ggtgaataca	gctgcttcca	tcaattttacc	tctccacaat	cagagaacaa	gaagcaacaa	4920
tttgcaaat	gggcgtgggt	tataaaaatta	gaacaacatt	taaaagaaaa	gaaaaatgca	4980
gatccttcta	attcttatac	tgcaacatta	cacgcaaaa	gtaccaaaaa	aatcgcccaa	5040
aaagtggggg	aagaaggtgt	ggaaactgcc	ttggctgcgg	tcgcacaaga	taaaagcgaa	5100
gtcatttctg	aagctacaga	tttgggtctat	cacttaaccg	tattattaca	caatcaagat	5160
cttcatgtgt	acgaaattat	cgcaaaaacta	caagaacgcc	atcaagggat	tggattacat	5220
ccagaaggag	gaaataaata	agaaaattgt	caggcaatat	taagttagca	attagaagat	5280
ttgtttgggc	aattcaatat	catcgtaaaa	tacagtgaat	ctatggtaat	taaatgtatt	5340
gataaacac	aaaatttagg	aaatatcatt	ttattccttc	ttcttaagca	acaatatagc	5400
aaggaagata	gtaaaaaatt	cacaatttat	aaattttatt	tacagactgt	aaattataca	5460
atacaattat	cgtaaaatttt	ttattacatc	ataaggaaac	aaaaatgaac	aaaactgtag	5520
gcagcacact	tcttgttgct	ggtacgatga	ttggcgcggg	aatgttggct	atgccactca	5580
cttcgcgtgg	cattggcttc	ggctttactt	tagtcttggt	attggggctt	tgggcattat	5640
taacttttag	cgacttttta	ttcgttgaa	tctatcaaac	tcggaagagt	gatgcaggta	5700
tcggcacact	tcgagaacaa	tatttttggt	aaacaggacg	cattattgcc	acagccgtgc	5760
taattatttt	cttatacgca	tttaattgcc	cttataatcag	cggtggcggt	tcactactaa	5820
aagattttat	accagaaagt	tttggcgata	aagttagcgt	cttattattt	accgtgattt	5880
tcggttcatt	tattgtcatc	ggcacacata	gcgtagataa	aattaatcgc	gtgttatttt	5940
tcgttatgct	tgctgccttt	gccgtgggtg	taagcttaat	gttgccagaa	atcaaatttg	6000
ataacttaat	ggcgacgcca	attgataagg	ctttaattat	ctctgcaagc	cctgtatttt	6060
tcacggcatt	tggtttccac	ggttccattc	caagttttaa	taaatactta	gatggcaatg	6120
taaaagcatt	gcgcttctct	atttttgctg	gctctgccat	aacactttgt	gcttatattc	6180
tatggcaact	atccacgcac	ggcttgctta	cacaaaatga	attttttaca	atcttaaaag	6240
aagatgcgac	tttaaatggc	ttagtaaaag	caaccttcgc	catcactgga	agcaatgtga	6300
tcgcaagtgc	ggtaaaatta	ttttctacat	tagcacttat	cacttctttc	ttaggtgtgg	6360
gattaggatt	attagaatgt	attgaagatt	tactaaaacg	ttcattttaac	gttacagcag	6420
gtagaatttc	acttggttta	ctgactttta	ttccaccact	tgtttttgca	ttattttacc	6480
cagaagggtt	tatttttagca	ctaggctacg	cagggtcaaat	gtttgcatte	tacgccgtag	6540
tattgccagt	tagccttggt	tggaaagctc	gtcgtgccca	cgctaatttg	ccatacaaag	6600
tgtgggggag	aaatctgact	ttaattatcg	tattggtatt	aggcgtgctc	attacatcca	6660

ttccatttgc	gattcgtgcg	ggttattttac	cctttgttgt	aggttaaaaa	caaactaaaa	6720
atttaccgca	ctttttatct	aaaaaagagt	aaatatgtgc	ctaattaatt	tagataaaaa	6780
tttcagacaa	aactttatcat	taatctttata	caacaaaaag	gctaagttct	aaaatttatag	6840
aacttagccc	ttaaactaaa	tgaagttcac	ttcatctata	ttatactttc	aattatcgtc	6900
ttgttttcaa	tagtttttca	gtgagttcat	aagctcgaag	ttttgctaac	tcttttagaaa	6960
gttttgcac	aagtaagtcg	tgatctgcat	cagatccgcg	agatactata	ttttcttctg	7020
ctttacgttt	tgcttcgtga	atacgatctg	catctaattc	actacctcga	atagcaatat	7080
ctgctaatac	tgtcacaata	tttggttgaa	cttctaaaaa	accaccagaa	acatagataa	7140
cttcttcatt	cccatcttta	agagtaaatt	taacaatccc	aggcttaatt	gctgtagca	7200
atggcgatg	tccgggcaaa	ataccaagct	ccccttccac	accagttacc	tgaatttggt	7260
ttacttcacc	ttcaaagatt	ttctgctctg	cgcttactat	tgttaaatta	aatgtcgcca	7320
ttttgtttct	cttcaaatga	cttgaagtga	ttacatat	ttggcttttt	ctaacacttc	7380
atcgattgaa	ccaaccatat	agaacgcttg	ttcaggaata	tggtcatatt	cgccatctaa	7440
gatacctttg	aagccacgga	tggtgtcttt	taatgtcacg	tatttacctg	gtgaacctgt	7500
gaagacttct	gcaacaaaga	atgggtgtga	taagaaacgt	tcaattttac	gtgcacgtgc	7560
taccactagt	tatatcttct	cagataattc	atccatacca	agaattgcga	taatatcttt	7620
caattcttta	taacgttgta	aaataccttg	tacaccacga	gcaacatcat	aatgttcttg	7680
accaacaaca	agcgggtcta	gctgacgtga	agttgaatct	aatggatcaa	ctgcagggtga	7740
aatacctaaa	gatgcgattt	gacgacttaa	tacaacagtt	gagtctaaat	gtgcgaaagt	7800
tggtgctgga	gatgggtcag	ttaagtcatc	cgctggtacg	tacaccgctt	gcacagaagt	7860
gatagaacct	gttttggttg	aagtgatagc	ttcttgtaac	acacccattt	cttctgcca	7920
tgtcggttg	taacctaccg	cggatggcat	acgacctaat	aacgcagata	cttccgtacc	7980
agcaagggtga	taacgataga	tattatccac	aaagaataat	acatctcgac	cttcatcacg	8040
gaatttttca	gccatagtta	aaccagtcaa	tgcaaacagt	aaacggttac	ctgggtgctc	8100
gttcatttga	ccataaacca	aagatacttt	atctaatacg	ttagaatctt	tcatttcatg	8160
atagaagtca	ttaccttcac	gagtacgttc	gcctacaccc	gcaaatacag	agtaacctga	8220
atgctcaatc	gcaatattac	gaatcaactc	catcatat	acggttttac	ctacacctgc	8280
accgccgaat	aaaccaactt	taccaccttt	tgcgaaatgga	caaattaagt	cgatcacttt	8340
gataccagtt	tctaataaatt	ccgtactggt	tgattgttct	tcatagctcg	gtgccgaacg	8400
gtggatagcc	caacgctctt	cttcaccaat	tgctccttgt	tcgtcaattg	gttcgcccaa	8460
cacattcata	atacgaccaa	gtgtttttgt	gcctactggt	acttgaattg	ggttatttgt	8520
gttttctact	tttaagccac	gttttaaac	atcagatgta	cccaatgcaa	tacaacgaac	8580
tactccgcca	cctaattgtt	gttgcactc	aagtgttaaa	cctgattcaa	cttttaatgc	8640
atcgtaaact	tttggcactg	catcttggtg	aaattcaacg	tcaatcacccg	caccgatgat	8700
ttgtacaatt	tttctgtctg	acattaccgt	tcctcttttc	ttaaatcgcc	gccgcaccgg	8760
ctacgatttc	attcaattca	tttgtgatac	ttgcttgacg	agctttgttg	tacaccaacc	8820
gcagatcatt	aattaaatta	cctgcattat	ccgttgctgc	tttcattgct	accattcgag	8880
ccgcttggtc	tgaagctaca	ttatctacaa	ccgcttgata	aatttgggac	tctaataaac	8940
gaactaaaag	gctatcta	agtacttttg	gttctggctc	ataaagataa	tcccaagtct	9000
tgtgtctttc	atttaaatga	tcgtctttag	attctggtaa	aggaactaat	tggtgtacaa	9060
caggcttttg	cgacatcgta	ttaacaaa	tattgtatgc	aatataaact	gcatcaattt	9120
caccattacg	ataagcatca	aacattgtat	ttgccacacc	aattaattct	tctagagcgg	9180
gcgtatcgcc	taaaccagaa	agctgacctt	tgatattaaa	tccaaaggaa	cggaaaaaac	9240
taatcccttt	tgaacctatt	aagcccaa	ctgtagaaat	attttgttct	ttccaatttt	9300
ttatttggtt	aagtgtggtt	ttgaataaat	taacatttaa	cccaccacac	atcccacgat	9360
ctgttgaaat	aaccaagata	ccgattttct	tcacttcgcg	ctcaactaag	aacggatggt	9420
tataaccgat	acttgcttta	gacacatgac	taataacggt	acggatagtt	tcagaatacg	9480
gacgagatgc	agccatacga	tcctgcgttt	tacgcatttt	cgagggtgcc	accatttcca	9540
ttgccttagt	gtacttttgt	gtactttgtg	cactggcaat	tttggttttt	atctcttttg	9600
cacctgccat	cttatctctc	cgttactacc	aagcactatt	cgctttaaaa	ccatctaaaa	9660
tactttttta	agtatctttg	atctcatcat	tatagttacc	ggttttatta	agctcttgca	9720
taaattcagc	gtgattacgg	ttagaataat	ctaaaagtgc	ggtctcaaaa	cttgcaattt	9780
ttgataattc	cacgtcatcc	aaataacc	attcaacagc	aaacaatata	accgcttggt	9840
ctgcaacaga	taatggcgtg	aattgttttt	gttttaataa	ttcagttact	ttttcaccgt	9900
gagaaagtgt	cttacgagtc	gcatcatcta	gatctgatgc	aaactgtgca	aacgctgcta	9960
attcacgata	ttgagctagc	gcggtacgaa	taccaccgcg	taatttctta	ataactttag	10020
tttgcgctga	accaccaaca	cgagataccg	aaataacctg	gtttaccgca	ggacgaatac	10080
ctgagttaaa	caagttagat	tctaagaaga	tctgaccatc	ggtaatagaa	attacgttgg	10140
ttggaacaaa	cgcagatacg	tcaccagctt	gggtttcaat	aatcggaagt	gcggttaaag	10200
aacctgtttt	tcctttttact	tcgcctttag	tgaatttttc	tacataatct	tcattttacac	10260
gagaagcacg	ttctagtaaa	cgagaatgta	aatagaacac	atcacctgga	taggcttcac	10320
gacctggtgg	acgacgtaat	aataatgaaa	tttgacgata	agctacggct	tgttttgata	10380
aatcatcata	aacaattaac	gcactcttcgc	cgcgatcacg	gaaatatcc	cccatcgcac	10440
aaccagcata	aggggctaaa	tattgtaacg	ctgctgattc	agatgcagat	gcagctacca	10500
cgatagtatt	tgcaagcgca	ccatgttctt	ctaatttacg	cacgacattt	gcaatagtag	10560

aggctttttg	accaatcgca	acatagatac	atttaatacc	tgaattacgt	tgattaataa	10620
tagcgtcaat	tgctaacgca	gttttaccgc	tttgacggtc	accgatgatt	aactcacgct	10680
gaccacgacc	aatcgggtacc	atagaatcga	cagctttata	accagtttga	acaggttgat	10740
caacagaacg	acgatcgata	acacctggcg	caatcacttc	tactgggtgag	aaaccatcat	10800
tttcaatttc	gcctttacca	tcgattggct	gaccaagcgt	attaactaca	cgacctataa	10860
aaccacgacc	aactgggtact	tcaagaatac	gacctgtaca	ttgaacttcc	ataccttccg	10920
ctaaatctgc	gtaaggtccc	ataactacag	caccaacaga	atcgcggttca	aggttaagtg	10980
ccatcgcata	acgattacct	ggtaaggcga	tcattttcacc	ttgcatcaca	tcgcttaaac	11040
cgtggatgcg	aataatacca	tcgcttacag	aaacaattgt	ccctgtatta	cgcgcttcac	11100
tgaccacgtc	gaattgagcg	atgcgttttt	taatcaattc	actaatttca	gttgaattta	11160
gttgcatctt	gtattcctct	tataattgca	actcgtttgc	aagacgagta	agttgccac	11220
ggctacttcc	gtcaatcaca	aagtcttcag	tacgaacaat	cacaccagca	ataagtgcgt	11280
tatccacggt	gcaatttaat	ttcactttgc	gagctaattc	tttttccatt	gcagctgcaa	11340
ttttttcgat	ttgtgttgca	ttcaatgggt	gcgcagatgt	tacttcaact	tctgcaatag	11400
cttggtgttc	ctctacgtga	tgtttaaat	cttcaaacac	cgcaggaata	gcactcaaac	11460
gcttattttc	agccattaac	cgaataagat	tttgcccata	ttgatccaat	tgttcgcac	11520
aaatagaaat	tactgtatca	gctaatttct	gtgcagaaag	agaactactt	aagtaagctt	11580
ttaccgtttc	atcttcagct	acggcagcag	caaaacctaa	catttcagtc	catttttcga	11640
ccgcactttg	ttcaatggca	aagtcgaatg	cagcttttgc	ataagggcga	gctattgtag	11700
ttaattctga	cataagctaa	gcctcttata	actctgcaac	taatttatca	ataatgtcat	11760
tgtttgccgc	ttcatcaata	gaacgaccca	caattttctc	agcaccagcc	actgccaatg	11820
aagctacttt	aagacgtaat	tcttcttgaa	caggtttacg	ttctgcttct	acttcagcat	11880
aaccttgtgc	aataattttt	gcttttagtt	cttcggcttc	tgcttcaact	tcgtctaata	11940
cttcattgcg	acgtttattc	gcagcatcta	aaatgtcttg	agcttgtaat	tttgacgtg	12000
aaagtctctg	ttcaacaaga	tttttcgtat	ctgcttgctc	ttttttagct	gcttcagctg	12060
acgctaaagc	gttcgcaatt	tggctttgac	gtgtttcaat	cgcattaata	attggtggcc	12120
aaacaaactt	catgcaaac	cacacgaaaa	gtgcgaatgc	gataagttga	ccaatcaatg	12180
ttgcatttaa	attcacaacg	tcctccttac	tatgcttggt	ttacgttgat	aagcaataa	12240
ggtgattagt	ttaataaacc	gatgaatggg	tttgcgaaaa	tgaaaagtaa	tgaaatacca	12300
acagcaatca	ttgcaatcgc	atctaaaaga	ccagctacga	taaacatttt	agtttgtaag	12360
ctagatgcta	attctggttg	gcgagctgat	gattctaaga	atttaccacc	tagaatagca	12420
aagccaattg	cagttaacct	tgcaagaaat	gcaagaagaa	ttgatgcacc	gatgattggt	12480
gctgtaatta	cagtttccat	aattttctcc	aatagaagtt	aagtttttagc	cttagagccg	12540
gttaataaaa	aacgattaat	gatctgcttt	gttataagca	atacttaaat	aaacaaccgt	12600
caacatcata	aagatgaaag	cctgcaaggt	aataaccaa	atatggaaaa	tagcccaagc	12660
aagatgtaac	ggaatcccta	atgctgcaat	ggccatatta	gcggaataca	ttacagcgat	12720
aagaataaag	atcaactccc	ctgcatacat	gttaccgaat	aaacggaagg	caagtgaat	12780
tggttttagcc	aataaagtca	ccgtttcaag	aataaaatta	acaggaataa	acgcccattg	12840
attgaatgga	tgaagcgtat	attcttttaac	taaacctttg	aatcctttag	attttattgt	12900
ataaaaaaga	attaaaaaga	aaacacaaat	ggacataccc	aaagtgcgc	taatatctgc	12960
tgctcgacat	gcacgaagat	aatgaatacc	gaacaaacct	gcaaattgag	gtaagaaatc	13020
aacaggaatt	aagtcatag	cattcatgat	gaatacccaa	cagaaaattg	ttaatgcaag	13080
tggcgcaact	acgttacgtg	gaccatgaaa	attttctttc	acgattccat	taaccatttc	13140
cacaacaatt	tcaactaagc	attgcatttt	tcctggaacg	ccagttgttg	cttttttccc	13200
tactcgagaa	aaaacaaata	ggaaaataac	cgcagcaaga	atagaaaaga	acaacgtatc	13260
tatatgaaca	ttccaaaatc	catcccctgt	tttgagaaag	gataaatggt	ggctaattgta	13320
ttccgatggt	gtttgtccag	acataatcga	tcctttgttc	tgaagaagaa	taacccaaag	13380
ttaaatttta	ttgagaataa	gtggaataat	attattcagc	actaatgcca	ataaaaaacc	13440
aacaaaaaac	gcaataaaat	tgataacgaa	taaccatttg	atggcaataa	tgataaaaaac	13500
catcggttaa	ataaacctta	ttgcttcagc	acgataaagt	cgggtcagtt	ttgttgaaaa	13560
attttgtttt	ctgtaaaaaa	tgataaatat	aaatgtacaa	aaaggcaaaa	aggcacttaa	13620
aaaaccgtag	ctaaaatcta	ccgcactttg	gcgttgccat	ccataaataa	gcaataaaaa	13680
aactacaagc	aaaagactct	caataacaat	agcttttctg	tagttttttt	tagcgtgaga	13740
taaaatgcgc	gacatcactt	ttacaaaata	attttagccc	gccgattata	cctttgctgg	13800
ctttagattc	aacttaaaaa	cacataaa				13828

//

```

ID   AF032869    standard; DNA; PRO; 307 BP.
XX
AC   AF032869;
XX
SV   AF032869.1
XX
DT   24-NOV-1997 (Rel. 53, Created)
DT   30-NOV-1997 (Rel. 53, Last updated, Version 3)
XX
DE   Actinobacillus pleuropneumoniae ATP synthase gene, partial cds.
XX
KW   .
XX
OS   Actinobacillus pleuropneumoniae
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Actinobacillus.
XX
RN   [1]
RP   1-307
RA   Bacmeister C.X., Fenwick B.W.;
RT   ;
RL   Submitted (03-NOV-1997) to the EMBL/GenBank/DDBJ databases.
RL   Diagnostic Medicine/Pathobiology, Kansas State University, 1800 Denison
RL   Ave, Manhattan, KS 66506-5605, USA
XX
DR   SPTREMBL; O31195; O31195.
XX
FH   Key          Location/Qualifiers
FH
FT   source          1..307
FT                       /db_xref="taxon:715"
FT                       /organism="Actinobacillus pleuropneumoniae"
FT                       /strain="4074"
FT                       /serotype="1"
FT   CDS            1..>307
FT                       /codon_start=1
FT                       /db_xref="SPTREMBL:O31195"
FT                       /transl_table=11
FT                       /product="ATP synthase"
FT                       /protein_id="AAB87466.1"
FT                       /translation="MATGKIVQIIIGAVIDVEFPQDAVPKVYDALKVESGLTLEVQQQLG
FT                       GGLVRCIALGTSDGLKRGLKVENTGNPIQVPVGTKTLGRIMNVLGEPIDEKGPIGEV"
XX
SQ   Sequence 307 BP; 97 A; 54 C; 79 G; 77 T; 0 other;
      atggcaacag gaaaaattgt acagattatc ggtgcggtaa tgcacgttga attcccgcaa      60
      gatgcagtac caaaagtata tgatgcctta aaagttgaat cgggtttaac ccttgaggtt      120
      caacaacaat taggtggtgg acttgtgcgt tgtatcgcat taggtacatc agacggttta      180
      aaacgcggct taaaagttga aaatacgggt aacccgattc aagtaccggt cggtacaaag      240
      actctgggtc gtattatgaa cgtattaggt gagccaatcg atgaaaaagg ccctatcggc      300
      gaagtag                                           307
//

```